

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Lal, Preeti
Corley, Neil C.
Shah, Purvi
- (ii) TITLE OF THE INVENTION: HUMAN S-ADENOSYL-L-METHIONINE
METHYLTRANSFERASE
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0352 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: THP1PLB01
 - (B) CLONE: 10625

Met 1	Ala	Ser	Arg	Gly 5	Arg	Arg	Pro	Glu	His 10	Gly	Gly	Pro	Pro	Glu 15	Leu
Phe	Tyr	Asp	Glu	Thr	Glu	Ala	Arg	Lys 25	Tyr	Val	Arg	Asn 30	Ser	Arg	Met
Ile	Asp	Ile	Gln	Thr	Arg	Met	Ala 40	Gly	Arg	Ala	Leu	Glu 45	Leu	Leu	Tyr
Leu	Pro 50	Glu	Asn	Lys	Pro	Cys 55	Tyr	Leu	Leu	Asp	Ile 60	Gly	Cys	Gly	Thr
Gly 65	Leu	Ser	Gly	Ser	Tyr 70	Leu	Ser	Asp	Glu	Gly 75	His	Tyr	Trp	Val	Gly 80
Leu	Asp	Ile	Ser	Pro 85	Ala	Met	Leu	Asp 90	Glu	Ala	Val	Asp	Arg	Glu 95	Ile
Glu	Gly	Asp	Leu 100	Leu	Leu	Gly	Asp 105	Met	Gly	Gln	Gly	Ile 110	Pro	Phe	Lys
Pro	Gly	Thr	Phe 115	Asp	Gly	Cys	Ile 120	Ser	Ile	Ser	Ala	Val 125	Gln	Trp	Leu
Cys	Asn 130	Ala	Asn	Lys	Lys	Ser 135	Glu	Asn	Pro	Ala	Lys 140	Arg	Leu	Tyr	Cys
Phe 145	Phe	Ala	Ser	Leu	Phe 150	Ser	Val	Leu	Val	Arg 155	Gly	Ser	Arg	Ala	Val 160
Leu	Gln	Leu	Tyr	Pro 165	Glu	Asn	Ser	Glu	Gln 170	Leu	Glu	Leu	Ile	Thr 175	Thr
Gln	Ala	Thr	Lys 180	Ala	Gly	Phe	Ser 185	Gly	Gly	Met	Val	Val 190	Asp	Tyr	Pro
Asn	Ser	Ala 195	Lys	Ala	Lys	Lys	Phe 200	Tyr	Leu	Cys	Leu	Phe 205	Ser	Gly	Pro
Ser	Thr 210	Phe	Ile	Pro	Glu	Gly 215	Leu	Ser	Glu	Asn	Gln 220	Asp	Glu	Val	Glu
Pro 225	Arg	Glu	Ser	Val 230	Phe	Thr	Asn	Glu	Arg	Phe 235	Pro	Leu	Arg	Met	Ser
Arg	Arg	Gly	Met	Val 245	Arg	Lys	Ser	Arg	Ala 250	Trp	Val	Leu	Glu	Lys 255	Lys
Glu	Arg	His	Arg 260	Arg	Gln	Gly	Arg	Glu 265	Val	Arg	Pro	Asp 270	Thr	Gln	Tyr
Thr	Gly	Arg 275	Lys	Arg	Lys	Pro	Arg 280	Phe							

(2) INFORMATION FOR SEO ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PLB01
(B) CLONE: 10625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGTCGCAGGT	GTGCTGCTGA	GGCGTGAGAA	TGGCGTCCCG	CGGCCGGCGT	CCGGAGCATG	60
GCGGACCCCC	AGAGCTGTTT	TATGACGAGA	CAGAAGCCCG	GAAATACGTT	CGCAACTCAC	120
GGATGATTGA	TATCCAGACC	AGGATGGCTG	GGCGAGCATT	GGAGCTTCTT	TATCTGCCAG	180
AGAATAAGCC	CTGTTACCTG	CTGGATATTG	GCTGTGGCAC	TGGGCTGAGT	GGAAGTTATC	240
TGTCAGATGA	AGGGCACTAT	TGGGTGGGCC	TGGATATCAG	CCCTGCCATG	CTGGATGAGG	300
CTGTGGACCG	AAGACATAG	GGAGACCTGC	TGCTGGGGGA	TATGGGCCAG	GGCATCCCAT	360
TCAAGCCAGG	CAGATTTGAT	GTTTGCATCA	GCATTTCTGC	TGTGCAGTGG	CTCTGTAATG	420
CTAACAAGAA	GTCTGAAAAC	CCTGCCAAGC	GCTGTACTG	CTTTTTTTGT	TCTCTTTTTT	480

CTGTTCTCGT	CCGGGGATCC	CGAGCTGTCC	TGCAGCTGTA	CCCTGAGAAC	TCAGAGCAGT	540
TGGAGCTGAT	CACAACCCAG	GCCACAAAGG	CAGGCTTCTC	CGGTGGCATG	GTGGTAGACT	600
ACCCTAACAG	TGCCAAAGCA	AAGAAATCTT	ACCTCTGCTT	GTTTTCTGGG	CCTTCGACCT	660
TTATAACCAGA	GGGGCTGAGT	GAAAATCAGG	ATGAAGTTGA	ACCCAGGGAG	TCTGTGTTCA	720
CCAATGAGAG	GTTCCCATTA	AGGATGTGCA	GGCGGGGAAT	GGTGAGGAAG	AGTCGGGCAT	780
GGGTGCTGGA	GAAGAAGGAG	CGGCACAGGC	GCCAGGGCAG	GGAAGTCAGA	CCTGACACCC	840
AGTACACCGG	CCGCAAGCGC	AAGCCCGCT	TCTAAGTCAC	CACGCGGTTT	TGGAAAGGCA	900
CTTGCCTCTG	CACTTTTCTA	TATTGTTTCA	CTGACAAAGT	AGTATTTTAG	AAAAGTTCTA	960
AAGTTATAAA	AATGTTTTCT	GCAGTAAAAA	AAAAGTTCTC	TGGGCCGGGC	GTGTTGGCTC	1020
ACACCTGTAA	TCCCAGCACC	TTGGGAGGCT	GAGGTGGGAG	GATCATTGTA	GCCCAGGAGT	1080
TTGAGACCTG	CCTGGGCAAC	ATAATGAAAC	TTCCTTTCCA	GGGAGAAAAA	AAAAA	1135

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1065505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Ser	Phe	Lys	Val	Lys	Pro	Glu	His	Thr	Gly	Pro	Pro	Asp	Leu	1	5	10	15
Tyr	Tyr	Asn	Glu	Thr	Glu	Ala	Ala	Lys	Tyr	Ala	Ser	Asn	Ser	His	Ile	20	25	30	
Thr	Ala	Ile	Gln	His	Glu	Met	Ala	Glu	Arg	Ala	Leu	Glu	Leu	Leu	Ala	35	40	45	
Leu	Pro	Glu	Gly	Lys	Ser	Gly	Phe	Leu	Leu	Asp	Ile	Gly	Cys	Gly	Thr	50	55	60	
Gly	Met	Ser	Ser	Glu	Val	Ile	Leu	Asp	Ala	Gly	His	Met	Phe	Val	Gly	65	70	75	80
Val	Asp	Val	Ser	Arg	Pro	Met	Leu	Glu	Ile	Ala	Arg	Gln	Asp	Glu	Asp	85	90	95	
Leu	Glu	Ser	Gly	Asp	Phe	Ile	His	Gln	Asp	Met	Gly	Leu	Gly	Met	Pro	100	105	110	
Phe	Arg	Pro	Gly	Ser	Phe	Asp	Gly	Ala	Ile	Ser	Ile	Ser	Ala	Ile	Gln	115	120	125	
Trp	Leu	Cys	His	Ala	Asn	Ala	Ser	Asp	Glu	Asn	Pro	Arg	Lys	Arg	Leu	130	135	140	
Leu	Phe	Phe	Phe	Gln	Ser	Leu	Tyr	Gly	Cys	Leu	Gly	Arg	Gly	Ser	Arg	145	150	155	160
Ala	Val	Phe	Gln	Phe	Tyr	Pro	Glu	Asn	Asp	Glu	Gln	Cys	Asp	Leu	Ile	165	170	175	
Met	Gly	Gln	Ala	His	Lys	Ala	Gly	Phe	Asn	Gly	Gly	Leu	Val	Val	Asp	180	185	190	
Phe	Pro	Glu	Ala	Ala	Lys	Arg	Lys	Lys	Val	Tyr	Leu	Val	Leu	Met	Thr	195	200	205	
Gly	Gly	Val	Val	Gln	Leu	Pro	Gln	Ala	Leu	Thr	Glu	Asp	Gly	Glu	Glu	210	215	220	
Ser	Arg	Thr	Gln	Ile	Asp	Asn	Ala	Gly	Arg	Arg	Phe	Val	Trp	Asn	Ser	225	230	235	240
Arg	Lys	Asn	Glu	Lys	Val	Ala	Lys	Gly	Ser	Lys	Ala	Trp	Ile	Glu	Ala	245	250	255	
Lys	Arg	Gln	Arg	Gln	Ile	Lys	Gln	Gly	Arg	Asp	Val	Arg	His	Glu	Ser	260	265	270	

Lys Tyr Ser Gly Arg Lys Arg Lys Thr Lys Phe
275 280

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1907189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Arg	Pro	Glu	Glu	Leu	Ala	Pro	Pro	Glu	Ile	Phe	Tyr	Asn	Asp	1	5	10	15
Ser	Glu	Ala	His	Lys	Tyr	Thr	Gly	Ser	Thr	Arg	Val	Gln	His	Ile	Gln	20	25	30	
Ala	Lys	Met	Thr	Leu	Arg	Ala	Leu	Glu	Leu	Leu	Asn	Leu	Gln	Pro	Cys	35	40	45	
Ser	Phe	Ile	Leu	Asp	Ile	Gly	Cys	Gly	Ser	Gly	Leu	Ser	Gly	Glu	Ile	50	55	60	
Leu	Thr	Gln	Glu	Gly	Asp	His	Val	Trp	Cys	Gly	Leu	Asp	Ile	Ser	Pro	65	70	75	80
Ser	Met	Leu	Ala	Thr	Gly	Leu	Ser	Arg	Glu	Leu	Glu	Gly	Asp	Leu	Met	85	90	95	
Leu	Gln	Asp	Met	Gly	Thr	Gly	Ile	Pro	Phe	Arg	Ala	Gly	Ser	Phe	Asp	100	105	110	
Ala	Ala	Ile	Ser	Ile	Ser	Ala	Ile	Gln	Trp	Leu	Cys	Asn	Ala	Asp	Thr	115	120	125	
Ser	Tyr	Asn	Asp	Pro	Lys	Gln	Arg	Leu	Met	Arg	Phe	Phe	Asn	Thr	Leu	130	135	140	
Tyr	Ala	Ala	Leu	Lys	Lys	Gly	Gly	Lys	Phe	Val	Ala	Gln	Phe	Tyr	Pro	145	150	155	160
Lys	Asn	Asp	Asp	Gln	Val	Asp	Asp	Ile	Leu	Gln	Ser	Ala	Lys	Val	Ala	165	170	175	
Gly	Phe	Ser	Gly	Gly	Leu	Val	Val	Asp	Asp	Pro	Glu	Ser	Lys	Lys	Asn	180	185	190	
Lys	Lys	Tyr	Tyr	Leu	Val	Leu	Ser	Ser	Gly	Ala	Pro	Pro	Gln	Gly	Glu	195	200	205	
Glu	Gln	Val	Asn	Leu	Asp	Gly	Val	Thr	Met	Asp	Glu	Glu	Asn	Val	Asn	210	215	220	
Leu	Lys	Lys	Gln	Leu	Arg	Gln	Arg	Leu	Lys	Gly	Gly	Lys	Asp	Lys	Glu	225	230	235	240
Ser	Ala	Lys	Ser	Phe	Ile	Leu	Arg	Lys	Lys	Glu	Leu	Met	Lys	Arg	Arg	245	250	255	
Gly	Arg	Lys	Val	Ala	Lys	Asp	Ser	Lys	Phe	Thr	Gly	Arg	Lys	Arg	Arg	260	265	270	
His	Arg	Phe														275			